

**AMENDMENTS TO THE CLAIMS:**

Claim 254 is amended. Claims 141-167 and 254-160 are pending. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-140 (Cancelled.)

Claim 141. (Currently amended.) An isolated variant of a parent glucoamylase comprising a mutation of amino acid position 402 in the amino acid sequence ~~shown in SEQ ID NO:2, or at a corresponding position in a homologous glucoamylase having wherein said variant has at least 80% homology with the amino acid sequence shown in SEQ ID NO:2, and wherein said variant has glucoamylase activity.~~

Claim 142. (Currently amended.) The variant of claim 141, wherein said ~~homologous variant~~ glucoamylase has at least 90% homology to SEQ ID NO:2.

Claim 143. (Currently amended.) The variant of claim 141, wherein said ~~homologous variant~~ glucoamylase has at least 95% homology to SEQ ID NO:2.

Claim 144. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~mutation~~ substitution at position 1 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.~~

Claim 145. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~mutation~~ substitution at position 2 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.~~

Claim 146. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~substitution~~ mutation at position 3 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.~~

Claim 147. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~substitution~~ mutation at position 4 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.~~

Claim 148. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~substitution~~mutation at position 5 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a~~ corresponding position in said homologous glucosylase.

Claim 149. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~substitution~~mutation at position 6 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a~~ corresponding position in said homologous glucosylase.

Claim 150. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~substitution~~mutation at position 7 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a~~ corresponding position in said homologous glucosylase.

Claim 151. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~substitution~~mutation at position 8 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a~~ corresponding position in said homologous glucosylase.

Claim 152. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~substitution~~mutation at position 9 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a~~ corresponding position in said homologous glucosylase.

Claim 153. (Currently amended.) The variant of claim 254, wherein said variant comprises a ~~substitution~~mutation at position 11 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a~~ corresponding position in said homologous glucosylase.

Claim 154. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 10 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a~~ corresponding position in said homologous glucosylase.

Claim 155. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 12 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a~~ corresponding position in said homologous glucosylase.

Claim 156. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 13 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucosylase.~~

Claim 157. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 14 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucosylase.~~

Claim 158. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 15 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucosylase.~~

Claim 159. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 16 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucosylase.~~

Claim 160. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 17 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucosylase.~~

Claim 161. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 18 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucosylase.~~

Claim 162. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 19 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucosylase.~~

Claim 163. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 21 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucosylase.~~

Claim 164. (Currently amended.) The variant of claim 254, wherein said variant comprises a

mutation at position 22 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.~~

Claim 165. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 23 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.~~

Claim 166. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 24 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.~~

Claim 167. (Currently amended.) The variant of claim 254, wherein said variant comprises a mutation at position 25 in the amino acid sequence ~~shown in SEQ ID NO:2 or at a corresponding position in said homologous glucoamylase.~~

Claims 168-253 (Cancelled.)

Claim 254. (Currently amended.) An isolated variant of a parent glucoamylase comprising \_\_\_\_\_ a glucoamylase having:

at least 80% homology with amino acid sequence SEQ ID NO:2,

a substitution of an amino acid at a position corresponding to position 402 in amino acid sequence SEQ ID NO:2 and

a substitution of an one or more amino acids at one or more of the following amino acids in the amino acid sequence shown in SEQ ID NO:2 corresponding to an amino acid selected from the following group of amino acids (using in SEQ ID NO:2 for numbering):

1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 10, 12, 13, 14, 15, 16, 17, 18, 19, 21, 22, 23, 24, 25, 26, 28, 29, 31, 32, 33, 34, 35, 40, 41, 42, 43, 44, 45, 46, 47, 49, 51, 53, 56, 58, 60, 61, 62, 73, 74, 75, 76, 77, 78, 79, 80, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 109, 110, 111, 113, 114, 115, 117, 118, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 234, 235, 237, 238, 239, 240, 242, 243, 244, 245, 287, 288, 289, 290, 291, 292, 294, 295, 296, 298, 299, 300, 301, 303, 304, 308, 311, 314, 315, 316, 318, 319, 334, 335, 336, 337, 338, 339, 340, 341, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 384, 388, 390, 394, 397, 398, 399, 403, 404, 405, 406, 409, 412, 413, 414, 445, 446, 447, 448,

449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470; and wherein said variant has glucoamylase activity.

~~or at a corresponding position in a homologous glucoamylase having at least 80% homology with the amino acid sequence shown in SEQ ID NO:2, and wherein said variant has glucoamylase activity.:-~~

~~1, 2, 3, 4, 5, 6, 7, 8, 9, 11, 10, 12, 13, 14, 15, 16, 17, 18, 19, 21, 22, 23, 24, 25 and 402.~~

Claim 255 (Currently amended.) The variant of claim 254, wherein said ~~homologous-variant~~ glucoamylase has at least 90% homology to SEQ ID NO:2.

Claim 256. (Currently amended.) The variant of claim 254, wherein said ~~homologous-variant~~ glucoamylase has at least 95% homology to SEQ ID NO:2.

Claim 257 (Currently amended.) The variant of claim 254, wherein said ~~homologous-variant~~ glucoamylase has at least 97% homology to SEQ ID NO:2.

Claim 258. (Currently amended.) The variant of claim 254, wherein said ~~homologous-variant~~ glucoamylase has at least 99% homology to SEQ ID NO:2.

Claim 259 (Currently amended.) The variant of claim 141, wherein said ~~homologous-variant~~ glucoamylase has at least 97% homology to SEQ ID NO:2.

Claim 260. (Currently amended.) The variant of claim 141, wherein said ~~homologous-variant~~ glucoamylase has at least 99% homology to SEQ ID NO:2.